WE CLAIM:

1. One or more isolated and purified nucleic acid molecules, wherein each of the nucleic acid molecules comprises a sequence that specifically hybridizes to one ABC transporter gene.

2. The one or more nucleic acid molecules according to claim 1 wherein the nucleic acid molecules comprise a portion of the 3′ untranslated region of the ABC transporter gene.

3. A set of at least two nucleic acid molecules, wherein each of the nucleic acid molecules comprises a sequence that specifically hybridizes to one ABC transporter gene.

4. The set according to claim 3, wherein the set comprises at least 10 nucleic acid molecules.

5. The set according to claim 3, wherein the set comprises at least 20 nucleic acid molecules.

6. The set according to claim 3, wherein the set comprises at least 30 nucleic acid molecules.

7. The set according to claim 3, wherein the set comprises 48 nucleic acid molecules.

8. The set according to any one of claims 3-7, wherein the nucleic acid molecules comprise a portion of the 3′ untranslated region of the ABC transporter gene.

9. The one or more nucleic acid molecules according to claim 1 or 2, wherein the one or more nucleic acid molecules comprise a nucleic acid sequence selected from:

(a) the nucleic acid sequences as shown in SEQ ID NOS: 1 to 47 and Figures 1 to 47, wherein T can also be U;

(b) nucleic acid sequences complementary to (a);

(c) nucleic acid sequences which are homologous to (a) or (b); or

(d) a fragment of (a) to (c), which comprises a sequence that specifically hybridizes to one of the ABC transporter genes.

10. The set according to claim 8, wherein the nucleic acid molecules comprise a nucleic acid sequence selected from:

(a) the nucleic acid sequences as shown in SEQ ID NOS: 1 to 47 and Figures 1 to 47, wherein T can also be U;

(b) nucleic acid sequences complementary to (a);

(c) nucleic acid sequences which are homologous to (a) or (b); or

(d) a fragment of (a) to (c), which comprises a sequence that specifically hybridizes to one of the ABC transporter genes.

11. One or more pairs of primers for preparing the one or more nucleic acid molecules, according to claim 1 or 2.

12. One or more pairs of primers for preparing the nucleic acid molecules according to any one or claims 3-10.

13. The one or more pairs of primers according to claim 11 or 12, wherein the primers comprise a nucleic acid sequence selected from:

(a) a nucleic acid sequence as shown in SEQ ID NOS: 48 to 141 and Table 1, wherein T can also be U;

(b) nucleic acid sequences complementary to (a); or

(c) nucleic acid sequences which are homologous to (a) or (b).

14. One or more pairs of primers, wherein the primer pairs comprise a nucleic acid sequence selected from one or more of:

(a) one or more isolated and purified pairs of nucleic acid sequences selected from:

SEQ ID NO: 48 and SEQ ID NO: 49;
SEQ ID NO: 50 and SEQ ID NO: 51;
SEQ ID NO: 52 and SEQ ID NO: 53;
SEQ ID NO: 54 and SEQ ID NO: 55;
SEQ ID NO: 56 and SEQ ID NO: 57;
SEQ ID NO: 58 and SEQ ID NO: 59;
SEQ ID NO: 60 and SEQ ID NO: 61;
SEQ ID NO: 62 and SEQ ID NO: 63;
SEQ ID NO: 64 and SEQ ID NO: 65;
SEQ ID NO: 66 and SEQ ID NO: 67;
SEQ ID NO: 68 and SEQ ID NO: 69;
SEQ ID NO: 70 and SEQ ID NO: 71;
SEQ ID NO: 72 and SEQ ID NO: 73;

SEQ ID NO: 74 and SEQ ID NO: 75;
SEQ ID NO: 76 and SEQ ID NO: 77;
SEQ ID NO: 78 and SEQ ID NO: 79;
SEQ ID NO: 80 and SEQ ID NO: 81;
SEQ ID NO: 82 and SEQ ID NO: 83;
SEQ ID NO: 84 and SEQ ID NO: 85;
SEQ ID NO: 86 and SEQ ID NO: 87;
SEQ ID NO: 88 and SEQ ID NO: 89;
SEQ ID NO: 90 and SEQ ID NO: 91;
SEQ ID NO: 92 and SEQ ID NO: 93;
SEQ ID NO: 94 and SEQ ID NO: 95;
SEQ ID NO: 96 and SEQ ID NO: 97;
SEQ ID NO: 98 and SEQ ID NO: 99;
SEQ ID NO: 100 and SEQ ID NO: 101;
SEQ ID NO: 102 and SEQ ID NO: 103;
SEQ ID NO: 104 and SEQ ID NO: 105;
SEQ ID NO: 106 and SEQ ID NO: 107;
SEQ ID NO: 108 and SEQ ID NO: 109;
SEQ ID NO: 110 and SEQ ID NO: 111;
SEQ ID NO: 112 and SEQ ID NO: 113;
SEQ ID NO: 114 and SEQ ID NO: 115;
SEQ ID NO: 116 and SEQ ID NO: 117;
SEQ ID NO: 118 and SEQ ID NO: 119;
SEQ ID NO: 120 and SEQ ID NO: 121;
SEQ ID NO: 122 and SEQ ID NO: 123;
SEQ ID NO: 124 and SEQ ID NO: 125;
SEQ ID NO: 126 and SEQ ID NO: 127;
SEQ ID NO: 128 and SEQ ID NO: 129;
SEQ ID NO: 130 and SEQ ID NO: 131;
SEQ ID NO: 132 and SEQ ID NO: 133;
SEQ ID NO: 134 and SEQ ID NO: 135;
SEQ ID NO: 136 and SEQ ID NO: 137;
SEQ ID NO: 138 and SEQ ID NO: 139; and

SEQ ID NO: 140 and SEQ ID NO: 141;

(b) the nucleic acid sequences in (a) wherein T can also be U;

(c) nucleic acid sequences complementary to (a) or (b); and

(d) nucleic acid sequences which are homologous to (a), (b) or (c).

15. One or more nucleic acid molecules prepared using PCR and the one or more pairs of primers according to claim 14.

16. A method of detecting the expression of one or more ABC transporter genes expression:

(a) providing one or more nucleic acid molecules, each comprising a sequence that specifically hybridizes to one ABC transporter gene;

(b) providing transcription indicators from a test sample;

(c) allowing the transcription indicators to hybridize with said one or more nucleic acid molecules; and

(d) detecting an amount of hybridization of said transcription indicators with said one or more nucleic acid sequences,

wherein the amount of hybridization is indicative of the expression of one or more ABC transporter genes.

17. The method according to claim 16 wherein the one or more nucleic acid molecules comprising a sequence that specifically hybridizes to one ABC transporter gene comprise a nucleic acid sequence selected from:

(a) the nucleic acid sequences as shown in SEQ ID NOS: 1 to 47 and Figures 1 to 47, wherein T can also be U;

(b) nucleic acid sequences complementary to (a);

(c) nucleic acid sequences which are homologous to (a) or (b); or

(d) a fragment of (a) to (c), which comprises a sequence that specifically hybridizes to one of the ABC transporter genes.

18. The method according to claim 16, wherein the one or more nucleic acid molecules comprising a sequence that specifically hybridizes to one ABC transporter gene are prepared using PCR and the primer pairs according to claim 14.

19. The method according to any one of claims 16-18 wherein the transcription indicators are selected from the group consisting of transcripts of the gene or genes, cDNA reverse transcribed from the transcript, cRNA transcribed from the cDNA, DNA amplified from the genes, RNA transcribed from amplified DNA, and the like.

20. The method according to claim 19, wherein the transcription indicator is cDNA.

21. The method according to any one of claims 15-20, wherein the transcription indicator is labeled.

22. The method according to any one of claims 15-21, wherein the test sample is from a human.

23. The method according to any one of claims 15-22, wherein the test sample is selected from one or more of cells, cell lines, tissues and organisms.

24. The method according to any one of claims 15-22, wherein the test sample is a clinical sample.

25. The method according to any one of claims 15-24 performed in microarray format.

26. A microarray comprising one or more nucleic acid molecules arrayed on a substrate, wherein the one or more nucleic acid molecules are selected from those claimed in claim 1, 2 and 9.

27. A microarray comprising the set of two or more nucleic acid molecules according to any one of claims 3-8, arrayed on a substrate.

28. The microarray according to any one of claims 26-27 further comprising one or more control nucleic acid molecules arrayed on the substrate.

29. The microarray according to claim 18, wherein the one or more expression level controls is used.

30. The method according to any one of claims 16-25, further comprising the steps of:

a) generating a set of expression data from the detection of the amount of hybridization;

b) storing the data in a database; and

c) performing comparative analysis on the set of expression data, thereby analyzing ABC transporter gene expression.

31. A computer system comprising (a) a database containing information identifying the expression level of a set of genes comprising at least two ABC transporter genes; and b) a user interface to view the information.

32. The computer system according to claim 31, wherein the information identifying the expression level of a set of genes comprising at least two ABC

transporter genes is obtained using a method according to any one of claims 16-25 and 30.

33. A method for screening compounds for their effect on the expression of one or more ABC transporter genes comprising:

(a) exposing a test sample to one or more compounds;

(b) providing a transcription indicator from the test sample;

(c) providing one or more nucleic acid sequences, each comprising a sequence that specifically hybridizes to one ABC transporter gene;

(d) allowing said transcription inhibitor to hybridize with said one or more nucleic acid sequences; and

(e) detecting an amount of hybridization of said transcription indicator with said one or more nucleic acid sequences,

wherein the amount of hybridization is indicative of expression of the one or more ABC transporter gene expression.

34. The method according to claim 33 further comprises the steps of

(f) quantitatively or qualitatively comparing the amount of hybridization detected in step (e) with the amount of hybridization of transcription indicators from a control sample, thereby determining the effect of the one or more compounds on the expression of the one or more ABC transporter genes.

35. A method for screening compounds for their effect on the expression of one or more ABC transporter genes comprising:

(a) preparing an ABC transporter gene expression profile, using a method according to any one of claims 16-25 and 30, of a test sample that has been exposed to one or more compounds;

(b) preparing an ABC transporter gene expression profile, using a method according to any one of claims 16-25 and 30, of a control sample; and

(c) quantitatively or qualitatively comparing the gene expression profiles from (a) and (b),

wherein differential expression profiles in (a) and (b) is indicative of a compound having an effect on the expression of one or more ABC transporter genes.

36. The method according to claim 35, wherein if the expression of one or more of the ABC transporter genes in the test sample is increased compared to the control sample, then the efficacy of the one or more compounds may be decreased.

37. The method according to claim 36, wherein if the expression of one or more of ABC B1 (MDR1), ABC C1 (MRP1), ABC C2 (MRP2), and ABC G2 (BCRP) in the test sample is increased compared to the control sample, then the efficacy of the one or more compounds may be decreased.

38. The method according to claim 35, wherein if the expression of one or more of the ABC transporter genes in the test sample is decreased compared to the control sample, then the efficacy and/or toxicity of the one or more compounds may be increased.

39. The method according to claim 38, wherein if the expression of one or more of ABC B1 (MDR1), ABC C1 (MRP1), ABC C2 (MRP2), and ABC G2 (BCRP) in the test sample is decreased compared to the control sample, then the efficacy and/or toxicity of the one or more compounds may be increased.

40. A method of assessing the toxicity and/or efficacy of a compound in a subject comprising:

(a) preparing an ABC transporter gene expression profile, using a method according to any one of claims 16-25 and 30, of a test sample that has been exposed to the compound;

(b) preparing an ABC transporter gene expression profile, using a method according to any one of claims 16-25 and 30, of a control sample; and

(c) quantitatively or qualitatively comparing the gene expression profiles from (a) and (b),

wherein a difference in the ABC transporter gene expression profiles in (a) and (b) is indicative of the toxicity and/or efficacy of the compound.

41. A method for determining a change in ABC transporter gene expression profile for a compound in the presence of one or more different compounds comprising:

(a) preparing an ABC transporter gene expression profile, using a method according to any one of claims 16-25 and 30, of a test sample that has been exposed to the compound;

(b) preparing an ABC transporter gene expression profile, using a method according to any one of claims 16-25 and 30, of a test sample that has been exposed to the compound and the one or more different compounds; and

(c) quantitatively or qualitatively comparing the gene expression profile in (a) and (b),

wherein differential expression in (a) and (b) indicates that the ABC transporter gene expression profile of the compound changes in the presence of the one or more different compounds.

42. The method according to claim 41, wherein changes in the ABC transporter gene expression profile indicate the presence of drug-drug interactions.

43. The method according to any one of claims 33-42 wherein the amount of hybridization is detected over a period of time at specified time intervals.

44. A kit combining, in different combinations, a nucleic acid microarray according to any one of claims 26-29, reagents for use with the microarrays, signal detection and array-processing instruments, gene expression databases and analysis and database management software.

45. A relational database comprising ABC transporter gene expression profiles obtained using the method according to any one of claims 16-25, 30 and 33-43.

46. The database according to claim 45, further comprising information selected from the group consisting of sequence information, descriptive information about the gene associated with the sequence information and the clinical status of the test sample and/or its source.